

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Inouye, Sumiko
Hsu, Mei-Yin
Eagle, Susan
Inouye, Masayori
- (ii) TITLE OF INVENTION: Prokaryotic Reverse Transcriptase
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Weiser & Associates
(B) STREET: 230 South Fifteenth Street, Suite 500
(C) CITY: Philadelphia
(D) STATE: Pennsylvania
(E) COUNTRY: U.S.A.
(F) ZIP: 19102
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/269,118
(B) FILING DATE: 10-JUN-1994
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Weiser, Gerard J.
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(C) REFERENCE/DOCKET NUMBER: 377.5888P
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 640..2094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCATCCGCGC GGACACCCCC TCCTACGTGC CCCCCGACGC GGAGAGCGGC GTGGAGACGG	60
TGTACCGCGT TTCCCTGGAT GGTACCTGG TGGCGGTGGA GTGGGGCCCG CGCACGGGCT	120
CGCCGCGTCA CCAGCGGCTC TGGTTCGACT CGGATGCGGA AGCCCCCGGA GCCTACTTCG	180

CGCGCCTCGA GAAGTTGGCG GCTGACGGCT ACATCGACGC GGCCTCGGCA TTGGTCTAAA	240
CCCTTCAACC ACGGCTCGGC CGCCACGCGC GGCCGGCAGG ACAGGTGCGA CGAACAGACG	300
ACGACGTGCG CTTACGCGC GAGCAGCCGA GAGAGGTCCG GAGTGCATCA GCCTGAGCGC	360
CTCGAGCGGC GGAGCGGCGT TGCGCCGCTC CGGTTGGAAT GCAGGACACT CTCCGCAAGG	420
TAGCCTGTTC TTGGCTCTCT CCCTCCTAGG CACTACGGCC AGGGTGGGTA GCGGAGCCAA	480
CGACGCCACC GCCGTTTACC CACCCCGGCC GTAGTGCCTA GGAGGGGAGA GCCGGTGAGG	540
CTACCGTGCC CCAGGTAAGA TGGTGGTGCT TTCCCGGCCT CCGTCGACTG CTCGCGCCAT	600
GTCCCGTCTT CCATCGCCGC GCCCGCCCAA GGTGCAGAC ATG ACC GCC AGG CTG	654
Met Thr Ala Arg Leu	
1 5	
GAC CCG TTC GTC CCC GCA GCT TCG CCG CAG GCC GTG CCC ACG CCC GAG	702
Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala Val Pro Thr Pro Glu	
10 15 20	
CTC ACC GCT CCG TCG TCA GAC GCG GCC GCG AAG CGT GAA GCC CGC CGG	750
Leu Thr Ala Pro Ser Ser Asp Ala Ala Lys Arg Glu Ala Arg Arg	
25 30 35	
CTC GCG CAC GAA GCG TTG CTC GTC CGC GCG AAG GCC ATC GAC GAA GCG	798
Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala Ile Asp Glu Ala	
40 45 50	
GGC GGC GCC GAC GAC TGG GTG CAG GCG CAG CTC GTC TCC AAG GGG CTC	846
Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val Ser Lys Gly Leu	
55 60 65	
GCG GTC GAG GAC CTG GAC TTC TCC AGC GCC TCC GAG AAG GAC AAG AAG	894
Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu Lys Asp Lys Lys	
70 75 80 85	
GCC TGG AAG GAG AAG AAG AAG GCC GAG GCC ACC GAG CGC CGC GCG CTG	942
Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Leu	
90 95 100	
AAG CGT CAG GCG CAC GAG GCG TGG AAG GCC ACG CAC GTG GGC CAC CTG	990
Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His Val Gly His Leu	
105 110 115	
GGC GCG GGC GTG CAC TGG GCG GAG GAC CGC CTG GCC GAC GCG TTC GAC	1038
Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu Ala Asp Ala Phe Asp	
120 125 130	
GTG CCC CAC CGC GAG GAG CGC GCC CGG GCC AAC GGC CTG ACG GAG CTG	1086
Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn Gly Leu Thr Glu Leu	
135 140 145	
GAC TCC GCG GAG GCG CTG GCC AAG GCG CTG GGG CTG AGC GTC TCC AAG	1134
Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly Leu Ser Val Ser Lys	
150 155 160 165	
CTC CGC TGG TTC GCG TTC CAC CGG GAG GTC GAC ACG GCC ACG CAC TAC	1182
Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr	
170 175 180	

GTG AGC TGG ACC ATT CCG AAG CGG GAC GGC AGC AAG CGC ACG ATT ACG Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr 185 190 195	1230
TCC CCC AAG CCT GAG CTG AAG GCA GCG CAG CGC TGG GTG CTG TCC AAC Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn 200 205 210	1278
GTC GTG GAG CGG CTG CCG GTC CAC GGC GCC GCC CAC GGC TTC GTG GCG Val Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala 215 220 225	1326
GGA CGC TCC ATC CTC ACC AAC GCG CTG GCC CAC CAG GGC GCG GAC GTC Gly Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val 230 235 240 245	1374
GTG GTC AAG GTG GAC CTC AAG GAC TTC TTC CCC TCC GTC ACC TGG CGC Val Val Lys Val Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg 250 255 260	1422
CGG GTG AAG GGC CTG TTG CGC AAG GGC GGC CTG CCG GAG GGC ACG TCC Arg Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser 265 270 275	1470
ACG CTG CTG TCC CTC CTC TCC ACG GAA GCG CCG CCG GAG GCG GTC CAG Thr Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln 280 285 290	1518
TTC CGC GGC AAG CTC CTG CAC GTC GCC AAG GGC CCG CGC GCC CTG CCC Phe Arg Gly Lys Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro 295 300 305	1566
CAG GGC GCC CCC ACG TCG CCC GGC ATC ACC AAC GCG CTC TGC CTG AAG Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys 310 315 320 325	1614
CTC GAC AAG CGG CTG TCC GCC CTC GCG AAG CGG CTG GGC TTC ACC TAC Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr 330 335 340	1662
ACG CGC TAC GCG GAC GAC CTG ACC TTC TGG ACG AAG GCG AAG CAG Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln 345 350 355	1710
CCC AAG CCG CGG CGG ACG CAG CGT CCC CCC GTC GCG GTC CTC CTG TCT Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser 360 365 370	1758
CGC GTC CAG GAA GTG GTG GAG GCG GAG GGC TTC CGC GTG CAC CCG GAC Arg Val Gln Glu Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp 375 380 385	1806
AAG ACG CGC GTC GCC CGC AAG GGC ACG CGG CAG CGG GTC ACC GGG CTC Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu 390 395 400 405	1854
GTC GTG AAT GCG GCG GGC AAG GAC GCG CCC GCG GCC CGA GTC CCG CGC Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg 410 415 420	1902
GAC GTC GTC CGC CAG CTC CGC GCC GCC ATC CAC AAC CGG AAG AAG GGC Asp Val Val Arg Gln Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly 425 430 435	1950

AAG CCG GGC CGC GAG GGC GAG TCG CTC GAG CAG CTC AAG GGC ATG GCC	1998
Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala	
440 445 450	
GCC TTC ATC CAC ATG ACG GAC CCG GCC AAG GGC CGC GCC TTC CTG GCT	2046
Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala	
455 460 465	
CAG CTC ACG GAG CTC GAG TCC ACG GCG AGC GCC GCT CCG CAG GCG GAG	2094
Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu	
470 475 480 485	
TGACGCTCAG CGCGCGTCCG TCGCCGACGT GCCGCGCGCC AGCAACGCGC CATTTCAGCAA	2154
CTCCGTCAGC CGGCGCGGGT AC	2176

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro	
1 5 10 15	
Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met	
20 25 30	
Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn	
35 40 45	
Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys	
50 55 60	
Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu	
65 70 75 80	
Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser	
85 90 95	
Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp	
100 105 110	
Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn	
115 120 125	
Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp	
130 135 140	
Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu	
145 150 155 160	
Pro Phe Lys Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp	
165 170 175	

Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys
 180 185 190
 Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro
 195 200 205
 Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu
 210 215 220
 Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys
 225 230 235 240
 Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn
 245 250 255
 Trp Ala Ser Gln Ile Tyr Pro
 260

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Pro Trp Ala Arg Thr Pro Pro Lys Ala Pro Arg Asn Gln Pro Val
 1 5 10 15
 Pro Phe Lys Pro Glu Arg Leu Gln Ala Leu Gln His Leu Val Arg Lys
 20 25 30
 Ala Leu Glu Ala Gly His Ile Glu Pro Tyr Thr Gly Pro Gly Asn Asn
 35 40 45
 Pro Val Phe Pro Val Lys Lys Ala Asn Gly Thr Trp Arg Phe Ile His
 50 55 60
 Asp Leu Arg Ala Thr Asn Ser Leu Thr Ile Asp Leu Ser Ser Ser Ser
 65 70 75 80
 Pro Gly Pro Pro Asp Leu Ser Ser Leu Pro Thr Thr Leu Ala His Leu
 85 90 95
 Gln Thr Ile Asp Leu Arg Asp Ala Phe Phe Gln Ile Pro Leu Pro Lys
 100 105 110
 Gln Phe Gln Pro Tyr Phe Ala Phe Thr Val Pro Gln Gln Cys Asn Tyr
 115 120 125
 Gly Pro Gly Thr Arg Tyr Ala Trp Lys Val Leu Pro Gln Gly Phe Lys
 130 135 140
 Asn Ser Pro Thr Leu Phe Glu Met Gln Leu Ala His Ile Leu Gln Pro
 145 150 155 160
 Ile Arg Gln Ala Phe Pro Gln Cys Thr Ile Leu Gln Tyr Met Asp Asp
 165 170 175

Ile Leu Leu Ala Ser Pro Ser His Glu Asp Leu Leu Leu Leu Ser Glu
 180 185 190
 Ala Thr Met Ala Ser Leu Ile Ser His Gly Leu Pro Val Ser Glu Asn
 195 200 205
 Lys Thr Gln Gln Thr Pro Gly Thr Ile Lys Phe Leu Gly Gln Ile Ile
 210 215 220
 Ser Pro Asn His Leu Thr Tyr Asp Ala Val Pro Thr Val Pro Ile Arg
 225 230 235 240
 Ser Arg Trp Ala Leu Pro Glu Leu Gln Ala Leu Leu Gly Glu Ile Gln
 245 250 255
 Trp Val Ser Lys Gly Thr Pro
 260

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr
 1 5 10 15
 Ile Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp
 20 25 30
 Arg Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys
 35 40 45
 Arg Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe
 50 55 60
 Gly Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg
 65 70 75 80
 Gly Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser
 85 90 95
 Phe Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe
 100 105 110
 Leu Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr
 115 120 125
 Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn
 130 135 140
 Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys
 145 150 155 160
 Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr
 165 170 175

Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly
 180 185 190
 Val Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe
 195 200 205
 Glu Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln
 210 215 220
 Glu Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys
 225 230 235 240
 Tyr Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly
 245 250 255
 Glu Tyr Lys

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr Val Ser Trp Thr
 1 5 10 15
 Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr Ser Pro Lys Pro
 20 25 30
 Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn Val Val Glu Arg
 35 40 45
 Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly Arg Ser Ile
 50 55 60
 Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val Val Lys Val
 65 70 75 80
 Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg Arg Val Lys Gly
 85 90 95
 Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser Thr Leu Leu Ser
 100 105 110
 Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln Phe Arg Gly Lys
 115 120 125
 Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro Gln Gly Ala Pro
 130 135 140
 Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys Leu Asp Lys Arg
 145 150 155 160
 Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr Thr Arg Tyr Ala
 165 170 175

Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln Pro Lys Pro Arg
 180 185 190
 Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser Arg Val Gln Glu
 195 200 205
 Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp Lys Thr Arg Val
 210 215 220
 Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu Val Val Asn Ala
 225 230 235 240
 Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg Asp Val Val Arg
 245 250 255
 Gln Leu Arg Ala Ala Ile His Asn Arg Lys
 260 265

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Thr Pro Glu Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys Arg
 1 5 10 15
 Glu Ala Arg Arg Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala
 20 25 30
 Ile Asp Glu Ala Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val
 35 40 45
 Ser Lys Gly Leu Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu
 50 55 60
 Lys Asp Lys Lys Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu
 65 70 75 80
 Arg Arg Ala Leu Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His
 85 90 95
 Val Gly His Leu Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu
 100 105 110

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Asp Pro Asp Met Thr Arg Val Thr Asn Ser Pro Ser Leu Gln Ala
1 5 10 15
His Leu Gln Ala Leu Tyr Leu Val Gln His Glu Val Trp Arg Pro Leu
20 25 30
Ala Ala Ala Tyr Gln Glu Gln Leu Asp Arg Pro Val Val Pro His Pro
35 40 45
Tyr Arg Val Gly Asp Thr Val Trp Val Arg Arg His Gln Thr Lys Asn
50 55 60
Leu Glu Pro Arg Trp Lys Gly Pro Tyr Thr Val Leu Leu Thr Thr Pro
65 70 75 80
Thr Ala Leu Lys Val Asp Gly Ile Ala Ala Trp Ile His Ala Ala His
85 90 95
Val Lys Ala Ala Asp Pro Gly Gly Gly Pro Ser Ser Arg Leu
100 105 110

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg Asp Val Val Arg Gln
1 5 10 15
Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly Lys Pro Gly Arg Glu
20 25 30
Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala Ala Phe Ile His Met
35 40 45
Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala Gln Leu Thr Glu Leu
50 55 60
Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Lys Glu Gly His Ser Ala Arg Gln Cys Arg Ala Pro Arg Arg Gln
1 5 10 15
Gly Cys Trp Lys Cys Gly Lys Pro Gly His Ile Met Thr Asn Cys Pro
20 25 30
Asp Arg Gln Ala Gly Phe Leu Gly Leu Gly Pro Trp Gly Lys Lys Pro
35 40 45
Arg Asn Phe Pro Val Ala Gln Val Pro Gln Gly Leu Thr Pro Thr Ala
50 55 60
Pro Pro
65

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Pro Arg Ala Leu Pro Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr
1 5 10 15
Asn Ala Leu Cys Leu Lys Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys
20 25 30
Arg Leu Gly Phe Thr Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser
35 40 45
Trp Thr Lys Ala Lys Gln Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro
50 55 60
Val Ala Val Leu
65

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Tyr Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser
1 5 10 15
Asn Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys
20 25 30

Lys Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser
35 40 45

Thr Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu
50 55 60

Gly Val Val Leu
65

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Lys Asn Leu Leu Pro Gln Gly Ala Pro Ser Ser Pro Lys Leu Ala
1 5 10 15

Asn Leu Ile Cys Ser Lys Leu Asp Tyr Arg Ile Gln Gly Tyr Ala Gly
20 25 30

Ser Arg Gly Leu Ile Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Leu Ser
35 40 45

Ala Gln Ser Met Lys Lys Val Val Lys Ala Arg Asp Phe Leu Phe Ser
50 55 60

Ile Ile Pro Ser
65

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile
1 5 10 15

Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Lys Lys Gln Asn
20 25 30

Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser
35 40 45

Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln
50 55 60

His Leu Leu
65

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Tyr Ala Trp Lys Val Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu
1 5 10 15
Phe Glu Met Gln Leu Ala His Ile Leu Gln Pro Ile Arg Gln Ala Phe
20 25 30
Pro Gln Cys Thr Ile Leu Gln Tyr Met Asp Asp Ile Leu Leu Ala Ser
35 40 45
Pro Ser His Glu Asp Leu Leu Leu Ser Glu Ala Thr Met Ala Ser
50 55 60
Leu Ile
65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Thr Trp Thr Arg Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu
1 5 10 15
Phe Asp Glu Ala Leu His Arg Asp Leu Ala Asp Phe Arg Ile Gln His
20 25 30
Pro Asp Leu Ile Leu Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala
35 40 45
Thr Ser Glu Leu Asp Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr
50 55 60
Leu
65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Phe Gln Trp Lys Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile
1 5 10 15
Cys Gln Leu Val Val Gly Gln Val Leu Glu Pro Leu Arg Leu Lys His
20 25 30
Pro Ser Leu Cys Met Leu His Tyr Met Asp Asp Leu Leu Leu Ala Ala
35 40 45
Ser Ser His Asp Gly Leu Glu Ala Ala Gly Glu Glu Val Ile Ser Thr
50 55 60
Leu
65

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Ala Trp Arg Val Leu Pro Gln Gly Phe Ile Asn Ser Pro Ala Leu
1 5 10 15
Phe Glu Arg Ala Leu Gln Glu Pro Leu Arg Gln Val Ser Ala Ala Phe
20 25 30
Ser Gln Ser Leu Leu Val Ser Tyr Met Asp Asp Ile Leu Tyr Ala Ser
35 40 45
Pro Thr Glu Glu Gln Arg Ser Gln Cys Tyr Gln Ala Leu Ala Ala Arg
50 55 60
Leu
65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ile Ala Thr Asn Gly Val Pro Gln Gly Ala Ser Thr Ser Cys Gly Leu
1 5 10 15

Ala Thr Tyr Asn Val Leu Glu Leu Phe Leu Arg Tyr Asp Glu Leu Ile
20 25 30

Met Tyr Ala Asp Asp Gly Ile Leu Cys Arg Gln Asp Pro Ser Thr Pro
35 40 45

Asp Phe Ser Val Glu Glu Ala Gly Val Val Gln Glu Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr Glu Tyr Leu Arg Met Pro Phe Gly Leu Lys Asn Ala Pro Ala Thr
1 5 10 15

Phe Gln Arg Cys Met Asn Asp Ile Leu Arg Pro Leu Leu Asn Lys His
20 25 30

Cys Leu Val Tyr Leu Asp Asp Ile Ile Val Phe Ser Thr Ser Leu Asp
35 40 45

Glu His Leu Gln Ser Leu Gly Leu Val Phe Glu Lys Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Glu Phe Cys Arg Leu Pro Phe Gly Leu Arg Asn Ala Ser Ser Ile
1 5 10 15

Phe Gln Arg Ala Leu Asp Asp Val Leu Arg Glu Gln Ile Gly Lys Ile
20 25 30

Cys Tyr Val Tyr Val Asp Asp Val Ile Ile Phe Ser Glu Asn Glu Ser
35 40 45

Asp His Val Arg His Ile Asp Thr Val Leu Lys Cys Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Cys Lys Leu Asn Lys Ala Ile Tyr Gly Leu Lys Gln Ala Ala Arg Cys
1 5 10 15
Trp Phe Arg Cys Ile Tyr Ile Leu Asp Lys Gly Asn Ile Asn Glu Asn
20 25 30
Ile Tyr Val Leu Leu Tyr Val Asp Asp Val Val Ile Ala Thr Gly Asp
35 40 45
Met Thr Arg Met Asn Asn Phe Lys Arg Tyr Leu Met Glu Lys Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Leu Leu Lys Lys Ser Leu Tyr Gly Leu Lys Gln Ser Pro Arg Gln
1 5 10 15
Trp Asn Ala Cys Val Tyr Val Lys Gln Val Ser Glu Gln Glu His Leu
20 25 30
Tyr Leu Leu Leu Tyr Val Asp Asp Met Leu Ile Ala Gly Lys Ser Lys
35 40 45
Ser Glu Ile Asn Lys Val Lys Glu Gln Leu Ser Met Glu Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile Arg Leu Lys Lys Ser Leu Tyr Glu Leu Lys Gln Ser Gly Ala Asn
1 5 10 15
Trp Tyr Glu Glu Val Arg Gly Trp Ser Cys Val Phe Lys Asn Ser Gln
20 25 30
Val Thr Ile Cys Leu Phe Val Asp Asp Met Val Leu Phe Ser Lys Asn
35 40 45
Leu Asn Ser Asn Lys Arg Ile Ile Glu Lys Leu Lys Met Gln Tyr
50 55 60

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "The 2' position of this nucleotide is linked to the 5' position of nucleotide number 1 of SEQ ID NO: 25 of this application."

(ix) FEATURE:

- (A) NAME/KEY: misc_binding
- (B) LOCATION: 52..58
- (D) OTHER INFORMATION: /note= "This region can hydrogen bond to nucleotides 61-67 of SEQ ID NO: 25 of this application."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CACGCAUGUA GGCAGAUUUG UUGGUUGUGA AUCGCAACCA GUGGCCUUA UGGCAGGA

58

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "The 5' position of this nucleotide is linked to the 2' position of nucleotide number 15 of SEQ ID NO: 24 of this application."

(ix) FEATURE:

- (A) NAME/KEY: misc binding
- (B) LOCATION: 61..67
- (D) OTHER INFORMATION: /note= "This region can hydrogen bond to nucleotides 52-58 of SEQ ID NO: 24 of this application."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTTCGCAC AGCACACCTG CCGTATAGCT CTGAATCAAG GATTTTAGGG AGGCGATTCC 60
TCCTGCC 67

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 418..2175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGCCATTNA GATACGGATT TTCACTTCCT TGACAGTGCA TGA CTATGCT GCATGAAATN 60
GCATGATCGA TTGAGGATCG TCTTTGCTCA GATCCGCCAG AACTGGCGGG CTTTGTCTCA 120
TGTCATGCAT GTGCATGAAA ACCACTGCAT AAAGCGGGCA GGCGTGCGG GGATACGAGC 180
GCGCGCTATC ACCGAAAATA GCCAAAATAC TTCTGGAAAA CAGAAAGTTG AAGTGATATG 240
TTCATAAACA CGCATGTAGG CAGATTTGTT GGTGTGTAAT CGCAACCAGT GGCCTTAATG 300
GCAGGAGGAA TCGCCTCCCT AAAATCCTTG ATTCAGAGCT ATACGGCAGG TGTGCTGTGC 360
GAAGGAGTGC CTGCATGCGT TTCTCCTTGG CCTTTTTTCC TCTGGGATGA AGAAGAA 417
ATG ACA AAA ACA TCT AAA CTT GAC GCA CTT AGG GCT GCT ACT TCA CGT 465
Met Thr Lys Thr Ser Lys Leu Asp Ala Leu Arg Ala Ala Thr Ser Arg
1 5 10 15
GAA GAC TTG GCT AAA ATT TTA GAT ATT AAG TTG GTA TTT TTA ACT AAC 513
Glu Asp Leu Ala Lys Ile Leu Asp Ile Lys Leu Val Phe Leu Thr Asn
20 25 30
GTT CTA TAT AGA ATC GGC TCG GAT AAT CAA TAC ACT CAA TTT ACA ATA 561
Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr Ile
35 40 45
CCG AAG AAA GGA AAA GGG GTA AGG ACT ATT TCT GCA CCT ACA GAC CGG 609
Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp Arg
50 55 60
TTG AAG GAC ATC CAA CGA AGA ATA TGT GAC TTA CTT TCT GAT TGT AGA 657
Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys Arg
65 70 75 80

GAT GAG ATC TTT GCT ATA AGG AAA ATT AGT AAC AAC TAT TCC TTT GGT Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe Gly	705
85 90 95	
TTT GAG AGG GGA AAA TCA ATA ATC CTA AAT GCT TAT AAG CAT AGA GGC Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg Gly	753
100 105 110	
AAA CAA ATA ATA TTA AAT ATA GAT CTT AAG GAT TTT TTT GAA AGC TTT Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser Phe	801
115 120 125	
AAT TTT GGA CGA GTT AGA GGA TAT TTT CTT TCC AAT CAG GAT TTT TTA Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe Leu	849
130 135 140	
TTA AAT CCT GTG GTG GCA ACG ACA CTT GCA AAA GCT GCA TGC TAT AAT Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr Asn	897
145 150 155 160	
GGA ACC CTC CCC CAA GGA AGT CCA TGT TCT CCT ATT ATC TCA AAT CTA Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn Leu	945
165 170 175	
ATT TGC AAT ATT ATG GAT ATG AGA TTA GCT AAG CTG GCT AAA AAA TAT Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys Tyr	993
180 185 190	
GGA TGT ACT TAT AGC AGA TAT GCT GAT GAT ATA ACA ATT TCT ACA AAT Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr Asn	1041
195 200 205	
AAA AAT ACA TTT CCG TTA GAA ATG GCT ACT GTG CAA CCT GAA GGG GTT Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly Val	1089
210 215 220	
GTT TTG GGA AAA GTT TTG GTA AAA GAA ATA GAA AAC TCT GGA TTC GAA Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe Glu	1137
225 230 235 240	
ATA AAT GAT TCA AAG ACT AGG CTT ACG TAT AAG ACA TCA AGG CAA GAA Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln Glu	1185
245 250 255	
GTA ACG GGA CTT ACA GTT AAC AGA ATC GTT AAT ATT GAT AGA TGT TAT Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys Tyr	1233
260 265 270	
TAT AAA AAA ACT CGG GCG TTG GCA CAT GCT TTG TAT CGT ACA GGT GAA Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly Glu	1281
275 280 285	
TAT AAA GTG CCA GAT GAA AAT GGT GTT TTA GTT TCA GGA GGT CTG GAT Tyr Lys Val Pro Asp Glu Asn Gly Val Leu Val Ser Gly Gly Leu Asp	1329
290 295 300	
AAA CTT GAG GGG ATG TTT GGT TTT ATT GAT CAA GTT GAT AAG TTT AAC Lys Leu Glu Gly Met Phe Gly Phe Ile Asp Gln Val Asp Lys Phe Asn	1377
305 310 315 320	
AAT ATA AAG AAA AAA CTG AAC AAG CAA CCT GAT AGA TAT GTA TTG ACT Asn Ile Lys Lys Lys Leu Asn Lys Gln Pro Asp Arg Tyr Val Leu Thr	1425
325 330 335	

AAT GCG ACT TTG CAT GGT TTT AAA TTA AAG TTG AAT GCG CGA GAA AAA	1473
Asn Ala Thr Leu His Gly Phe Lys Leu Lys Leu Asn Ala Arg Glu Lys	
340 345 350	
GCA TAT AGT AAA TTT ATT TAC TAT AAA TTT TTT CAT GGC AAC ACC TGT	1521
Ala Tyr Ser Lys Phe Ile Tyr Tyr Lys Phe Phe His Gly Asn Thr Cys	
355 360 365	
CCT ACG ATA ATT ACA GAA GGG AAG ACT GAT CGG ATA TAT TTG AAG GCT	1569
Pro Thr Ile Ile Thr Glu Gly Lys Thr Asp Arg Ile Tyr Leu Lys Ala	
370 375 380	
GCT TTG CAT TCT TTG GAG ACA TCA TAT CCT GAG TTG TTT AGA GAA AAA	1617
Ala Leu His Ser Leu Glu Thr Ser Tyr Pro Glu Leu Phe Arg Glu Lys	
385 390 395 400	
ACA GAT AGT AAA AAG AAA GAA ATA AAT CTT AAT ATA TTT AAA TCT AAT	1665
Thr Asp Ser Lys Lys Lys Glu Ile Asn Leu Asn Ile Phe Lys Ser Asn	
405 410 415	
GAA AAG ACC AAA TAT TTT TTA GAT CTT TCT GGG GGA ACT GCA GAT CTG	1713
Glu Lys Thr Lys Tyr Phe Leu Asp Leu Ser Gly Gly Thr Ala Asp Leu	
420 425 430	
AAA AAA TTT GTA GAG CGT TAT AAA AAT AAT TAT GCT TCT TAT TAT GGT	1761
Lys Lys Phe Val Glu Arg Tyr Lys Asn Asn Tyr Ala Ser Tyr Tyr Gly	
435 440 445	
TCT GTT CCA AAA CAG CCA GTG ATT ATG GTT CTT GAT AAT GAT ACA GGT	1809
Ser Val Pro Lys Gln Pro Val Ile Met Val Leu Asp Asn Asp Thr Gly	
450 455 460	
CCA AGC GAT TTA CTT AAT TTT CTG CGC AAT AAA GTT AAA AGC TGC CCA	1857
Pro Ser Asp Leu Leu Asn Phe Leu Arg Asn Lys Val Lys Ser Cys Pro	
465 470 475 480	
GAC GAT GTA ACT GAA ATG AGA AAG ATG AAA TAT ATT CAT GTT TTC TAT	1905
Asp Asp Val Thr Glu Met Arg Lys Met Lys Tyr Ile His Val Phe Tyr	
485 490 495	
AAT TTA TAT ATA GTT CTC ACA CCA TTG AGT CCT TCC GGC GAA CAA ACT	1953
Asn Leu Tyr Ile Val Leu Thr Pro Leu Ser Pro Ser Gly Glu Gln Thr	
500 505 510	
TCA ATG GAG GAT CTT TTC CCT AAA GAT ATT TTA GAT ATC AAG ATT GAT	2001
Ser Met Glu Asp Leu Phe Pro Lys Asp Ile Leu Asp Ile Lys Ile Asp	
515 520 525	
GGT AAG AAA TTC AAC AAA AAT AAT GAT GGA GAC TCA AAA ACG GAA TAT	2049
Gly Lys Lys Phe Asn Lys Asn Asn Asp Gly Asp Ser Lys Thr Glu Tyr	
530 535 540	
GGG AAG CAT ATT TTT TCC ATG AGG GTT GTT AGA GAT AAA AAG CGG AAA	2097
Gly Lys His Ile Phe Ser Met Arg Val Val Arg Asp Lys Lys Arg Lys	
545 550 555 560	
ATA GAT TTT AAG GCA TTT TGT TGT ATT TTT GAT GCT ATA AAA GAT ATA	2145
Ile Asp Phe Lys Ala Phe Cys Cys Ile Phe Asp Ala Ile Lys Asp Ile	
565 570 575	
AAG GAA CAT TAT AAA TTA ATG TTA AAT AGC TAATGAACAG CCCTAACGTT	2195
Lys Glu His Tyr Lys Leu Met Leu Asn Ser	
580 585	

ATGAACGCTA AGGCTGATTT TTCGTTAAAA TTTATATGGT TTGAATTGTA ATATATTATC 2255
 TTCAAGCCAT TTATTTAATT CCTGCATCCT TTTCTGTAAG GGTATTAATT CGTTCCTCAC 2315
 AAACACTAAA CTCGCTTTTT CCACATCCCC AAACCCCCT AACATTATTC GGCATAATCC 2375
 CCATCATTTG CGGTGGCACA CGATGCGCTG CCATCATGTC ATCGCGGC 2423

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro
 1 5 10 15
 Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met
 20 25 30
 Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn
 35 40 45
 Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys
 50 55 60
 Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu
 65 70 75 80
 Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser
 85 90 95
 Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp
 100 105 110
 Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn
 115 120 125
 Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp
 130 135 140
 Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu
 145 150 155 160
 Pro Phe Lys Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp
 165 170 175
 Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys
 180 185 190
 Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro
 195 200 205
 Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu
 210 215 220

Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys
 225 230 235 240
 Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn
 245 250 255
 Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys
 260 265 270
 Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu
 275 280 285
 Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro
 290 295 300
 Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile
 305 310 315 320
 Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro
 325 330 335
 Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His
 340 345 350
 Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr
 355 360 365
 Glu Ser Ile Val Ile Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile
 370 375 380
 Gln Lys Glu Thr Trp Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr
 385 390 395 400
 Trp Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu
 405 410 415
 Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr
 420 425 430
 Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr
 435 440 445
 Val Thr Asn Lys Gly Arg Gln Lys Val Val Pro Leu Thr Asn Thr Thr
 450 455 460
 Asn Gln Lys Thr Glu Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser
 465 470 475 480
 Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr Ala Leu Gln Ile
 485 490 495
 Ile Gln Ala Gln Pro Asp Lys Ser Glu Ser Glu Leu Val Asn Gln Ile
 500 505 510
 Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro
 515 520 525
 Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser
 530 535 540
 Ala Gly
 545

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Arg Pro Trp Ala Arg Thr Pro Pro Lys Ala Pro Arg Asn Gln Pro Val
1 5 10 15
Pro Phe Lys Pro Glu Arg Leu Gln Ala Leu Gln His Leu Val Arg Lys
20 25 30
Ala Leu Glu Ala Gly His Ile Glu Pro Tyr Thr Gly Pro Gly Asn Asn
35 40 45
Pro Val Phe Pro Val Lys Lys Ala Asn Gly Thr Trp Arg Phe Ile His
50 55 60
Asp Leu Arg Ala Thr Asn Ser Leu Thr Ile Asp Leu Ser Ser Ser Ser
65 70 75 80
Pro Gly Pro Pro Asp Leu Ser Ser Leu Pro Thr Thr Leu Ala His Leu
85 90 95
Gln Thr Ile Asp Leu Arg Asp Ala Phe Phe Gln Ile Pro Leu Pro Lys
100 105 110
Gln Phe Gln Pro Tyr Phe Ala Phe Thr Val Pro Gln Gln Cys Asn Tyr
115 120 125
Gly Pro Gly Thr Arg Tyr Ala Trp Lys Val Leu Pro Gln Gly Phe Lys
130 135 140
Asn Ser Pro Thr Leu Phe Glu Met Gln Leu Ala His Ile Leu Gln Pro
145 150 155 160
Ile Arg Gln Ala Phe Pro Gln Cys Thr Ile Leu Gln Tyr Met Asp Asp
165 170 175
Ile Leu Leu Ala Ser Pro Ser His Glu Asp Leu Leu Leu Leu Ser Glu
180 185 190
Ala Thr Met Ala Ser Leu Ile Ser His Gly Leu Pro Val Ser Glu Asn
195 200 205
Lys Thr Gln Gln Thr Pro Gly Thr Ile Lys Phe Leu Gly Gln Ile Ile
210 215 220
Ser Pro Asn His Leu Thr Tyr Asp Ala Val Pro Thr Val Pro Ile Arg
225 230 235 240
Ser Arg Trp Ala Leu Pro Glu Leu Gln Ala Leu Leu Gly Glu Ile Gln
245 250 255
Trp Val Ser Lys Gly Thr Pro Thr Leu Arg Gln Pro Leu His Ser Leu
260 265 270

Tyr Cys Ala Leu Gln Arg His Thr Asp Pro Arg Asp Gln Ile Tyr Leu
 275 280 285
 Asn Pro Ser Gln Val Gln Ser Leu Val Gln Leu Arg Gln Ala Leu Ser
 290 295 300
 Gln Asn Cys Arg Ser Arg Leu Val Gln Thr Leu Pro Leu Leu Gly Ala
 305 310 315 320
 Ile Met Leu Thr Leu Thr Gly Thr Thr Thr Val Val Phe Gln Ser Lys
 325 330 335
 Glu Gln Trp Pro Leu Val Trp Leu His Ala Pro Leu Pro His Thr Ser
 340 345 350
 Gln Cys Pro Trp Gly Gln Leu Leu Ala Ser Ala Val Leu Leu Leu Asp
 355 360 365
 Lys Tyr Thr Leu Gln Ser Tyr Gly Leu Leu Cys Gln Thr Ile His His
 370 375 380
 Asn Ile Ser Thr Gln Thr Phe Asn Gln Phe Ile Gln Thr Ser Asp His
 385 390 395 400
 Pro Ser Val Pro Ile Leu Leu His His Ser His Arg Phe Lys Asn Leu
 405 410 415
 Gly Ala Gln Thr Gly Glu Leu Trp Asn Thr Phe Leu Lys Thr Ala Ala
 420 425 430
 Pro Leu Ala Pro Val Lys Ala Leu Met Pro Val Phe Thr Leu Ser Pro
 435 440 445
 Val Ile Ile Asn Thr Ala Pro Cys Leu Phe Ser Asp Gly Ser Thr Ser
 450 455 460
 Arg Ala Ala Tyr Ile Leu Trp Asp Lys Gln Ile Leu Ser Gln Arg Ser
 465 470 475 480
 Phe Pro Leu Pro Pro Pro His Lys Ser Ala Gln Arg Ala Glu Leu Leu
 485 490 495
 Gly Leu Leu His Gly Leu Ser Ser Ala Arg Ser Trp Arg Cys Leu Asn
 500 505 510
 Ile Phe Leu Asp Ser Lys Tyr Leu Tyr His Tyr Leu Arg Thr Leu Ala
 515 520 525
 Leu Gly Thr Phe Gln Gly Arg Ser Ser Gln Ala Pro Phe Gln Ala Leu
 530 535 540
 Leu Pro Arg Leu Leu Ser Arg Lys Val Val Tyr Leu His His Val Arg
 545 550 555 560
 Ser His Thr Asn Leu Pro Asp Pro Ile Ser Arg Leu Asn Ala Leu Thr
 565 570 575
 Asp Ala

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr
1 5 10 15
Ile Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp
20 25 30
Arg Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys
35 40 45
Arg Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe
50 55 60
Gly Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg
65 70 75 80
Gly Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser
85 90 95
Phe Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe
100 105 110
Leu Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr
115 120 125
Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn
130 135 140
Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys
145 150 155 160
Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr
165 170 175
Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly
180 185 190
Val Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe
195 200 205
Glu Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln
210 215 220
Glu Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys
225 230 235 240
Tyr Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly
245 250 255
Glu Tyr Lys Val Pro Asp Glu Asn Gly Val Leu Val Ser Gly Gly Leu
260 265 270

Asp Lys Leu Glu Gly Met Phe Gly Phe Ile Asp Gln Val Asp Lys Phe
 275 280 285
 Asn Asn Ile Lys Lys Lys Leu Asn Lys Gln Pro Asp Arg Tyr Val Leu
 290 295 300
 Thr Asn Ala Thr Leu His Gly Phe Lys Leu Lys Leu Asn Ala Arg Glu
 305 310 315 320
 Lys Ala Tyr Ser Lys Phe Ile Tyr Tyr Lys Phe Phe His Gly Asn Thr
 325 330 335
 Cys Pro Thr Ile Ile Thr Glu Gly Lys Thr Asp Arg Ile Tyr Leu Lys
 340 345 350
 Ala Ala Leu His Ser Leu Glu Thr Ser Tyr Pro Glu Leu Phe Arg Glu
 355 360 365
 Lys Thr Asp Ser Lys Lys Lys Glu Ile Asn Leu Asn Ile Phe Lys Ser
 370 375 380
 Asn Glu Lys Thr Lys Tyr Phe Leu Asp Leu Ser Gly Gly Thr Ala Asp
 385 390 395 400
 Leu Lys Lys Phe Val Glu Arg Tyr Lys Asn Asn Tyr Ala Ser Tyr Tyr
 405 410 415
 Gly Ser Val Pro Lys Gln Pro Val Ile Met Val Leu Asp Asn Asp Thr
 420 425 430
 Gly Pro Ser Asp Leu Leu Asn Phe Leu Arg Asn Lys Val Lys Ser Cys
 435 440 445
 Pro Asp Asp Val Thr Glu Met Arg Lys Met Lys Tyr Ile His Val Phe
 450 455 460
 Tyr Asn Leu Tyr Ile Val Leu Thr Pro Leu Ser Pro Ser Gly Glu Gln
 465 470 475 480
 Thr Ser Met Glu Asp Leu Phe Pro Lys Asp Ile Leu Asp Ile Lys Ile
 485 490 495
 Asp Gly Lys Lys Phe Asn Lys Asn Asn Asp Gly Asp Ser Lys Thr Glu
 500 505 510
 Tyr Gly Lys His Ile Phe Ser Met Arg Val Val Arg Asp Lys Lys Arg
 515 520 525
 Lys Ile Asp Phe Lys Ala Phe Cys Cys Ile Phe Asp Ala Ile Lys Asp
 530 535 540
 Ile Lys Glu His Tyr Lys Leu Met Leu Asn Ser
 545 550 555

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Trp Phe Ser Phe His Arg Glu Val Asp Thr Gly Thr His Tyr Gln
1 5 10 15
Thr Trp Glu Ile Pro Lys Arg Asp Gly Gly Lys Arg Thr Leu Thr Ala
20 25 30
Pro Lys Arg Glu Leu Lys Ala Val Gln Arg Trp Val Leu Ala Asn Val
35 40 45
Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly
50 55 60
Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val
65 70 75 80
Val Lys Val Asp Met Lys Asp Phe Phe Pro Ser Val Thr Trp Pro Arg
85 90 95
Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Pro Glu Asn Leu Ala Thr
100 105 110
Leu Leu Ala Leu Leu Ser Thr Glu Ala Pro Arg Glu Val Val Arg Phe
115 120 125
Arg Gly Glu Thr Leu Tyr Val Ala Lys Gly Pro Arg Ala Leu Pro Gln
130 135 140
Gly Ala Pro Thr Ser Pro Ala Leu Thr Asn Ala Leu Cys Leu Arg Leu
145 150 155 160
Asp Lys Arg Leu Ser Ala Leu Ser Lys Arg Leu Gly Phe Thr Tyr Thr
165 170 175
Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Arg Arg Ala Lys Lys Ser
180 185 190
Arg Gln Lys Glu Leu Pro Leu Ala Asp Ala Pro Val Ala Leu Leu Leu
195 200 205
Ala Arg Val Lys Gly Val Leu Glu Ala Glu Gly Phe Thr Leu His Pro
210 215 220
Asp Lys Thr Arg Val Gln Arg Lys Gly Ser Arg Gln Arg Val Thr Gly
225 230 235 240
Leu Val Val

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Arg Trp Phe Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr Val
1 5 10 15
Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr Ser
20 25 30
Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn Val
35 40 45
Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly
50 55 60
Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val
65 70 75 80
Val Lys Val Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg Arg
85 90 95
Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser Thr
100 105 110
Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln Phe
115 120 125
Pro Arg Glu Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro Gln
130 135 140
Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys Leu
145 150 155 160
Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr Thr
165 170 175
Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln Pro
180 185 190
Lys Pro Arg Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser Arg
195 200 205
Val Gln Glu Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp Lys
210 215 220
Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu Val
225 230 235 240
Val

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Arg His Tyr Ser Ile His Arg Pro Arg Glu Arg Val Arg His Tyr Val
1 5 10 15
Thr Phe Ala Val Pro Lys Arg Ser Gly Gly Val Arg Leu Leu His Ala
20 25 30
Pro Lys Arg Arg Leu Lys Ala Leu Gln Arg Arg Met Leu Ala Leu Leu
35 40 45
Val Ser Lys Leu Pro Val Ser Pro Gln Ala His Gly Phe Val Pro Gly
50 55 60
Arg Ser Ile Lys Thr Gly Ala Ala Pro His Val Gly Arg Arg Val Val
65 70 75 80
Leu Lys Leu Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Phe Ala Arg
85 90 95
Val Arg Gly Leu Leu Lys Ala Leu Gly Tyr Gly Tyr Pro Val Ala Ala
100 105 110
Thr Leu Ala Val Leu Met Thr Glu Ser Glu Arg Gln Pro Val Glu Leu
115 120 125
Glu Gly Ile Leu Phe His Val Pro Val Gly Pro Arg Val Cys Val Gln
130 135 140
Gly Ala Pro Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu
145 150 155 160
Asp Arg Arg Leu Ala Gly Leu Ala Arg Arg Tyr Gly Tyr Thr Tyr Thr
165 170 175
Arg Tyr Ala Asp Asp Leu Thr Phe Ser Gly Asp Asp Val Thr Ala Leu
180 185 190
Glu Arg Val Arg Ala Leu Ala Ala Arg Tyr Val Gln Glu Glu Gly Phe
195 200 205
Glu Val Asn Arg Glu Lys Thr Arg Val Gln Arg Arg Gly Gly Ala Gln
210 215 220
Arg Val Thr Gly Val Thr Val
225 230

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Phe Leu Thr Asn Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr
1 5 10 15

Gln Phe Thr Ile Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala
 20 25 30
 Pro Thr Asp Arg Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu
 35 40 45
 Ser Asp Cys Arg Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn
 50 55 60
 Tyr Ser Phe Gly Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr
 65 70 75 80
 Lys His Arg Gly Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe
 85 90 95
 Phe Glu Ser Phe Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn
 100 105 110
 Gln Asp Phe Leu Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala
 115 120 125
 Ala Cys Tyr Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile
 130 135 140
 Ile Ser Asn Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu
 145 150 155 160
 Ala Lys Lys Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr
 165 170 175
 Ile Ser Thr Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln
 180 185 190
 Pro Glu Gly Val Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn
 195 200 205
 Ser Gly Phe Glu Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr
 210 215 220
 Ser Arg Gln Glu Val Thr Gly Leu Thr Val
 225 230

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Glu Thr Leu Arg Leu Leu Ile Tyr Thr Ala Asp Phe Arg Tyr Arg
 1 5 10 15
 Ile Tyr Thr Val Glu Lys Lys Gly Pro Glu Lys Arg Met Arg Thr Ile
 20 25 30
 Tyr Gln Pro Ser Arg Glu Leu Lys Ala Leu Gln Gly Trp Val Leu Arg
 35 40 45

Asn Ile Leu Asp Lys Leu Ser Ser Ser Pro Phe Ser Ile Gly Phe Glu
 50 55 60
 Lys His Gln Ser Ile Leu Asn Asn Ala Thr Pro His Ile Gly Ala Asn
 65 70 75 80
 Phe Ile Leu Asn Ile Asp Leu Glu Asp Phe Phe Pro Ser Leu Thr Ala
 85 90 95
 Asn Lys Val Phe Gly Val Phe His Ser Leu Gly Tyr Asn Arg Leu Ile
 100 105 110
 Ser Ser Val Leu Thr Lys Ile Cys Cys Tyr Lys Asn Leu Leu Pro Gln
 115 120 125
 Gly Ala Pro Ser Ser Pro Lys Leu Ala Asn Leu Ile Cys Ser Lys Leu
 130 135 140
 Asp Tyr Arg Ile Gln Gly Tyr Ala Gly Ser Arg Gly Leu Ile Tyr Thr
 145 150 155 160
 Arg Tyr Ala Asp Asp Leu Thr Leu Ser Ala Gln Ser Met Lys Lys Val
 165 170 175
 Val Lys Ala Arg Asp Phe Leu Phe Ser Ile Ile Pro Ser Glu Gly Leu
 180 185 190
 Val Ile Asn Ser Lys Lys Thr Cys Ile Ser Gly Pro Arg Ser Gln Arg
 195 200 205
 Lys Val Thr Gly Leu Val Ile
 210 215

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Lys Gly Phe Ala Ser Glu Val Met Arg Ser Pro Glu Pro Pro Lys
 1 5 10 15
 Lys Trp Asp Ile Ala Lys Lys Lys Gly Gly Met Arg Thr Ile Tyr His
 20 25 30
 Pro Ser Ser Lys Val Lys Leu Ile Gln Tyr Trp Leu Met Asn Asn Val
 35 40 45
 Phe Ser Lys Leu Pro Met His Asn Ala Ala Tyr Ala Phe Val Lys Asn
 50 55 60
 Arg Ser Ile Lys Ser Asn Ala Leu Leu His Ala Glu Ser Lys Asn Lys
 65 70 75 80
 Tyr Tyr Val Lys Ile Asp Leu Lys Asp Phe Phe Pro Ser Ile Lys Phe
 85 90 95

Thr Asp Phe Glu Tyr Ala Phe Thr Arg Tyr Arg Asp Arg Ile Glu Phe
 100 105 110
 Thr Thr Glu Tyr Asp Leu Glu Leu Leu Gln Leu Ile Lys Thr Ile Cys
 115 120 125
 Phe Ile Ser Asp Ser Thr Leu Pro Ile Gly Phe Pro Thr Ser Pro Leu
 130 135 140
 Ile Ala Asn Phe Val Ala Arg Glu Leu Asp Glu Lys Leu Thr Gln Lys
 145 150 155 160
 Leu Asn Ala Ile Asp Lys Leu Asn Ala Thr Tyr Thr Arg Tyr Ala Asp
 165 170 175
 Asp Ile Ile Val Ser Thr Asn Met Lys Gly Ala Ser Lys Leu Ile Leu
 180 185 190
 Asp Cys Phe Lys Arg Thr Met Lys Glu Ile Gly Pro Asp Phe Lys Ile
 195 200 205
 Asn Ile Lys Lys Phe Lys Ile Cys Ser Ala Ser Gly Gly Ser Ile Val
 210 215 220
 Val Thr Gly Leu Lys Val
 225 230

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ile Gln Arg Leu His Ala Leu Ser Asn His Ala Gly Arg His Tyr Arg
 1 5 10 15
 Arg Ile Ile Leu Ser Lys Arg His Gly Gly Gln Arg Leu Val Leu Ala
 20 25 30
 Pro Asp Tyr Leu Leu Lys Thr Val Gln Arg Asn Ile Leu Lys Asn Val
 35 40 45
 Leu Ser Gln Phe Pro Leu Ser Pro Phe Ala Thr Ala Tyr Arg Pro Gly
 50 55 60
 Cys Pro Ile Val Ser Asn Ala Gln Pro His Cys Gln Gln Pro Gln Ile
 65 70 75 80
 Leu Lys Leu Asp Ile Glu Asn Phe Phe Asp Ser Ile Ser Trp Leu Gln
 85 90 95
 Val Trp Arg Val Phe Arg Gln Ala Gln Leu Pro Arg Asn Val Val Thr
 100 105 110
 Met Leu Thr Trp Ile Cys Cys Tyr Asn Asp Ala Leu Pro Gln Gly Ala
 115 120 125

Pro Thr Ser Pro Ala Ile Ser Asn Leu Val Met Arg Arg Phe Asp Glu
 130 135 140
 Arg Ile Gly Glu Trp Cys Gln Ala Arg Gly Ile Thr Tyr Thr Arg Tyr
 145 150 155 160
 Cys Asp Asp Met Thr Phe Ser Gly His Phe Asn Ala Arg Gln Val Lys
 165 170 175
 Asn Lys Val Cys Gly Leu Leu Ala Glu Leu Gly Leu Ser Leu Asn Lys
 180 185 190
 Arg Lys Gly Cys Leu Ile Ala Ala Cys Lys Arg Gln Gln Val Thr Gly
 195 200 205
 Ile Val Val
 210

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1640 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 279..1559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTCCGAGCCC GCCTCCGAGG ACGCGCTCGC GGCCCGGGCG GCGGGGGCGG ACGCGCGGCG 60
 GCGGCCCCACG GAGACGCTTG ACCCGGGAGA CGACGAATGA CGATAACGGC AGGTGCTCTC 120
 GGGAGAGGCC AGGGCTCGCA GATGAGCCAT GAGTACCGCG GTGTTTCGCC GCGGGGGTGT 180
 TCTGTCCCCA TCTCTTCGCC AGGGTCCCAG CGTACGCAAC GCAGGGAGCC CCGGGTCCAA 240
 CGCCTCGCAG GTCGTCCCCT GGCCTCTTCC GGAGCACC ATG AGC TGG TTC GAC 293
 Met Ser Trp Phe Asp
 1 5
 ACC ACC CTC TCC CGG CTC AAG GGG TTG TTC AGC CGT CCC GTG ACA CGA 341
 Thr Thr Leu Ser Arg Leu Lys Gly Leu Phe Ser Arg Pro Val Thr Arg
 10 15 20
 AGC ACC ACC GGG CTG GAC GTG CCG CTG GAT GCC CAC GGA CGT CCC CAG 389
 Ser Thr Thr Gly Leu Asp Val Pro Leu Asp Ala His Gly Arg Pro Gln
 25 30 35
 GAC GTC GTG ACG GAG ACG GTC TCC ACG TCG GGC CCC CTG AAG CCA GGG 437
 Asp Val Val Thr Glu Thr Val Ser Thr Ser Gly Pro Leu Lys Pro Gly
 40 45 50
 CAC CTG CGA CAG GTC CGC CGG GAT GCG CGG CTG CTC CCC AAG GGC GTC 485
 His Leu Arg Gln Val Arg Arg Asp Ala Arg Leu Leu Pro Lys Gly Val
 55 60 65

CGC CGC TAC ACC CCG GGC CGG AAG AAG TGG ATG GAG GCC GCC GAG GCC	533
Arg Arg Tyr Thr Pro Gly Arg Lys Lys Trp Met Glu Ala Ala Glu Ala	
70 75 80 85	
CGG CGG CTG TTC TCC GCC ACG CTG CGC ACG CGG AAC CGG AAC CTG AGG	581
Arg Arg Leu Phe Ser Ala Thr Leu Arg Thr Arg Asn Arg Asn Leu Arg	
90 95 100	
GAC TTG CTG CCC GAC GAG GCA CAG CTG GCG CGC TAC GGC CTG CCG GTC	629
Asp Leu Leu Pro Asp Glu Ala Gln Leu Ala Arg Tyr Gly Leu Pro Val	
105 110 115	
TGG CGC ACG GAA GAG GAC GTG GCA GCG GCC CTG GGC GTC TCG GTG GGC	677
Trp Arg Thr Glu Glu Asp Val Ala Ala Ala Leu Gly Val Ser Val Gly	
120 125 130	
GTG CTC CGC CAC TAC AGC ATC CAC CGC CCG CGC GAG CGG GTG CGG CAC	725
Val Leu Arg His Tyr Ser Ile His Arg Pro Arg Glu Arg Val Arg His	
135 140 145	
TAC GTG ACC TTC GCC GTG CCC AAG CGC TCC GGA GGC GTC CGG CTG CTG	773
Tyr Val Thr Phe Ala Val Pro Lys Arg Ser Gly Gly Val Arg Leu Leu	
150 155 160 165	
CAT GCG CCC AAG CGG CGC CTG AAG GCC CTG CAA CGC CGG ATG CTG GCG	821
His Ala Pro Lys Arg Arg Leu Lys Ala Leu Gln Arg Arg Met Leu Ala	
170 175 180	
CTC CTG GTG TCG AAG CTC CCC GTG AGT CCA CAG GCC CAT GGC TTC GTG	869
Leu Leu Val Ser Lys Leu Pro Val Ser Pro Gln Ala His Gly Phe Val	
185 190 195	
CCC GGC CGC TCC ATC AAG ACG GGC GCC GCG CCG CAC GTG GGC CGG CGG	917
Pro Gly Arg Ser Ile Lys Thr Gly Ala Ala Pro His Val Gly Arg Arg	
200 205 210	
GTG GTC CTG AAG CTG GAC CTG AAG GAC TTC TTC CCC TCC GTC ACC TTC	965
Val Val Leu Lys Leu Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Phe	
215 220 225	
GCG CGG GTG CGA GGG CTG CTC ATC GCC CTG GGC TAC GGC TAT CCC GTG	1013
Ala Arg Val Arg Gly Leu Leu Ile Ala Leu Gly Tyr Gly Tyr Pro Val	
230 235 240 245	
GCG GCC ACG CTC GCG GTG CTG ATG ACG GAG TCC GAG CGC CAG CCC GTG	1061
Ala Ala Thr Leu Ala Val Leu Met Thr Glu Ser Glu Arg Gln Pro Val	
250 255 260	
GAG CTG GAG GGC ATC CTC TTC CAC GTT CCC GTG GGC CCA CGC GTC TGC	1109
Glu Leu Glu Gly Ile Leu Phe His Val Pro Val Gly Pro Arg Val Cys	
265 270 275	
GTG CAG GGC GCC CCC ACG AGC CCC GCC CTG TGC AAC GCG GTG CTG CTG	1157
Val Gln Gly Ala Pro Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu	
280 285 290	
CGA CTG GAC CGG CGG CTG GCG GGA CTG GCG CGT CGG TAC GGC TAC ACG	1205
Arg Leu Asp Arg Arg Leu Ala Gly Leu Ala Arg Arg Tyr Gly Tyr Thr	
295 300 305	
TAC ACG CGC TAC GCG GAT GAC CTC ACC TTC TCC GGC GAC GAC GTC ACG	1253
Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Gly Asp Asp Val Thr	
310 315 320 325	

GCG CTG GAG CGA GTC CGC GCG CTG GCC GCG CGG TAC GTG CAG GAG GAA	1301
Ala Leu Glu Arg Val Arg Ala Leu Ala Ala Arg Tyr Val Gln Glu Glu	
330 335 340	

GGC TTC GAG GTC AAC CGC GAG AAG ACC CGC GTG CAG CGC CGG GGC GGT	1349
Gly Phe Glu Val Asn Arg Glu Lys Thr Arg Val Gln Arg Arg Gly Gly	
345 350 355	

GCC CAG CGC GTC ACT GGC GTC ACC GTG AAT ACG ACG CTG GGC TTG TCA	1397
Ala Gln Arg Val Thr Gly Val Thr Val Asn Thr Thr Leu Gly Leu Ser	
360 365 370	

CGC GAG GAG CGG CCG CGG CTC CGG GCG ATG CTG CAC CAG GAG GCG CGG	1445
Arg Glu Glu Arg Pro Arg Leu Arg Ala Met Leu His Gln Glu Ala Arg	
375 380 385	

TCG GAG GAC GTC GAG GCA CAC CGC GCG CAC CTC GAC GGC CTC CTG GCC	1493
Ser Glu Asp Val Glu Ala His Arg Ala His Leu Asp Gly Leu Leu Ala	
390 395 400 405	

TAC GTG AAG ATG CTC AAC CCG GAG CAG GCG GAG CGG CTC GCT CGC CGG	1541
Tyr Val Lys Met Leu Asn Pro Glu Gln Ala Glu Arg Leu Ala Arg Arg	
410 415 420	

CGC AAG CCG CGC GGG ACG TGAGCGAGGG CTCAGCTCCG GATGGGCCAG	1589
Arg Lys Pro Arg Gly Thr	
425	

GGCCTGTCAC GCGTCCCGGC CTCCAGTTG TCATGGCGGC CGTCCAGTA C	1640
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(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 763..2202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCCCTTCCG GCGCTCGGGC TCGCGAGGG CCCGTGCGAG CACATGATGG CGCTGCGGCT	60
CGTCCAGGTC CGGCACCGCG CCGAGCAGGA AGCACTGCGT CAGACCCCCG CGGGCCGCCA	120
GCTCATCCGC GCGGAGACGC GCTCCTACGT GCGGCGCGAG CCCTCCGGCC AGGAGCAGGT	180
GTACCGCGTC TCATTGGATG GGAAAGTGGT GGCGGTGGAG TGGGGCCCCC GCCAGGGGGA	240
GTCCCGCCGG CAGAAGCTCT GGTTCGACAC GGACGCCGAG GCGCGACCG CCTACTTCAC	300
GCGCCTGGAG TCCTTGGCCG CGGAGGGATA TATCGATGCG GCTGCTTCAA TGATGTAGAA	360
CACGCAAGCC ACGGGCCGC GGGCGCGCGG CGGAAAGGCA GGTGCGACGG AACGACAGAC	420
ACTCGTGCGA GCGACCGAGA GAGGTCCCAA GCCATCAGCC TCAGCGCCTC GAGCGCGAGA	480
GCGGCGTTGC GCCGCTCTGG TTGAATTGCA GGACACTCTC CGCAAGGTAG CCTGTTCTTG	540

GCTCTCTTCC	CTCCGGTGAG	TACCTCTCCG	GCCGGGGAGC	TGAACCAACG	ACGCAACCGC	600
CGTTTCCCCG	GCCGGAGAGG	TACTCACC GG	AGGGGAGAGC	CGGTGAGGCT	ACCGTGCCCC	660
AGGTGAGAAG	GTGGTGCCTT	CGGGCCTCCC	TCGACCGCTC	GCGCTCCGTC	GCCCTGCCCT	720
GCCTCGCCCC	CCCCACCTTG	CTCACC GGCG	CCAGGAGCCG	TC ATG ACC GCC AAG		774
				Met Thr Ala Lys		
				1		
CTG GAG TCA CAC GTC CCC GCC GCG CCC CCC GTC TCC GCC GAG GCG CCC						822
Leu Glu Ser His Val Pro Ala Ala Pro Pro Val Ser Ala Glu Ala Pro						
5 10 15 20						
GCC CCC ACC CGT CCC GAT GCC GCG AAG CAG GAG GCC CGC CGC GCC CAC						870
Ala Pro Thr Arg Pro Asp Ala Ala Lys Gln Glu Ala Arg Arg Ala His						
25 30 35						
CAC GAG GCG CTG CGC CTG CGG TGG AAG GCC ATC GAA GAG GCG GGC GGC						918
His Glu Ala Leu Arg Leu Arg Trp Lys Ala Ile Glu Glu Ala Gly Gly						
40 45 50						
ACG GAC GCC TGG GTG CGG CAG CAG CTG GTG GCC AAG GGC GTC GCG GCG						966
Thr Asp Ala Trp Val Arg Gln Gln Leu Val Ala Lys Gly Val Ala Ala						
55 60 65						
GAA GAG GTG GAC TTC GAG TCG CTC AGC GAC AAG CAG AAG GCG GCC TGG						1014
Glu Glu Val Asp Phe Glu Ser Leu Ser Asp Lys Gln Lys Ala Ala Trp						
70 75 80						
AAG GAG AAG AAG AAG GCC GAG GCC ACC GAG CGG CGC GCG CAG AAG CGC						1062
Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Gln Lys Arg						
85 90 95 100						
CTG GCG TGG GAG GCC TGG AAG GCC ACG CAC ATC CAC CAC CTG GGC GTG						1110
Leu Ala Trp Glu Ala Trp Lys Ala Thr His Ile His His Leu Gly Val						
105 110 115						
GGG GTG CAC TGG GAC GAG GCC GGA GGG CCG GAC AAG TTC GAC GTG GCC						1158
Gly Val His Trp Asp Glu Ala Gly Gly Pro Asp Lys Phe Asp Val Ala						
120 125 130						
GGG CGC GAG GAG CGG GCC AAG GCC AAC GGC TTG CCG GAG GGG TTG GAC						1206
Gly Arg Glu Glu Arg Ala Lys Ala Asn Gly Leu Pro Glu Gly Leu Asp						
135 140 145						
TCG GTC GAG GCG CTG GCC AAA GCG CTG GGC ATC TCC GTG TCG CGC CTG						1254
Ser Val Glu Ala Leu Ala Lys Ala Leu Gly Ile Ser Val Ser Arg Leu						
150 155 160						
CGC TGG TTC TCC TTC CAC CGC GAG GTG GAC ACG GGC ACG CAC TAC CAG						1302
Arg Trp Phe Ser Phe His Arg Glu Val Asp Thr Gly Thr His Tyr Gln						
165 170 175 180						
ACG TGG GAG ATT CCG AAG CGG GAC GGC GGC AAG CGG ACG CTC ACC GCG						1350
Thr Trp Glu Ile Pro Lys Arg Asp Gly Gly Lys Arg Thr Leu Thr Ala						
185 190 195						
CCG AAG CGG GAG CTC AAG GCC GTG CAG CGC TGG GTG CTC GCG AAC GTG						1398
Pro Lys Arg Glu Leu Lys Ala Val Gln Arg Trp Val Leu Ala Asn Val						
200 205 210						

GTG GAG CGG CTG CCG GTG CAC GGG GCC GCG CAC GGC TTC GTG GCG GGG Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly 215 220 225	1446
CGC TCC ATC CTC ACC AAC GCG CTG GCC CAC CAG GGC GCG GAC GTG GTG Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val 230 235 240	1494
GTG AAG GTG GAC ATG AAG GAC TTC TTC CCT TCC GTG ACG TGG CCC CGG Val Lys Val Asp Met Lys Asp Phe Phe Pro Ser Val Thr Trp Pro Arg 245 250 255 260	1542
GTC AAG GGA CTG CTG CGC AAG GGA GGA CTC CCG GAG AAC CTG GCG ACG Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Pro Glu Asn Leu Ala Thr 265 270 275	1590
CTC CTG GCG CTG CTC TCC ACC GAG GCC CCG CGC GAG GTG GTG CCG TTC Leu Leu Ala Leu Leu Ser Thr Glu Ala Pro Arg Glu Val Val Arg Phe 280 285 290	1638
CGG GGA GAG ACG CTG TAC GTG GCC AAG GGC CCT CGC GCG CTG CCC CAG Arg Gly Glu Thr Leu Tyr Val Ala Lys Gly Pro Arg Ala Leu Pro Gln 295 300 305	1686
GGG GCC CCC ACC TCT CCG GCG CTG ACG AAC GCG CTG TGC CTG CGG CTG Gly Ala Pro Thr Ser Pro Ala Leu Thr Asn Ala Leu Cys Leu Arg Leu 310 315 320	1734
GAC AAG CGG CTC TCG GCG CTG TCG AAG CGG CTG GGC TTC ACG TAC ACG Asp Lys Arg Leu Ser Ala Leu Ser Lys Arg Leu Gly Phe Thr Tyr Thr 325 330 335 340	1782
CGC TAT GCG GAT GAC CTG ACG TTC TCC TGG CGG CGG GCG AAG AAG TCC Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Arg Arg Ala Lys Lys Ser 345 350 355	1830
CGG CAG AAG GAA CTC CCC CTG GCG GAT GCG CCG GTG GCG CTG CTC CTG Arg Gln Lys Glu Leu Pro Leu Ala Asp Ala Pro Val Ala Leu Leu Leu 360 365 370	1878
GCG CGG GTG AAG GGT GTG CTG GAG GCC GAG GGT TTC ACG CTG CAC CCG Ala Arg Val Lys Gly Val Leu Glu Ala Glu Gly Phe Thr Leu His Pro 375 380 385	1926
GAC AAG ACG CGG GTG CAG CGC AAG GGC AGC CGG CAG CGG GTG ACG GGG Asp Lys Thr Arg Val Gln Arg Lys Gly Ser Arg Gln Arg Val Thr Gly 390 395 400	1974
CTC GTG GTG AAC GAG GCC CCC GAG GGC GTT CCG GGT GCC CGG GTG CCC Leu Val Val Asn Glu Ala Pro Glu Gly Val Pro Gly Ala Arg Val Pro 405 410 415 420	2022
CGC GAT GTG GTG CGG CGG CTG CGC GCG GCG ATC CAC AAC CGG GAG CAG Arg Asp Val Val Arg Arg Leu Arg Ala Ala Ile His Asn Arg Glu Gln 425 430 435	2070
GGC AAG CCC GGC CCC ACC GGG GAG ACG CTG GAG CAG CTC AAG GGG CTC Gly Lys Pro Gly Pro Thr Gly Glu Thr Leu Glu Gln Leu Lys Gly Leu 440 445 450	2118
GCG GCC TTC CTT CAC ATG ACG GAC GCG GAG AAG GGC CGC GCC TTC CTG Ala Ala Phe Leu His Met Thr Asp Ala Glu Lys Gly Arg Ala Phe Leu 455 460 465	2166

CGA CGG CTG GAG GCC CTC GAG AAG CGC CAG ACC GCC TGACCCTCAC 2212
 Arg Arg Leu Glu Ala Leu Glu Lys Arg Gln Thr Ala
 470 475 480

TGGTCGTCCG GGGCATCGCA GCGGGCGCCG GGACGGACCG TCACCCCCCA GATCTCCATG 2272

CCATGCTGGG GATTCTGGGC GGTGAAGAAG ACTTCCCAGC CGAGACGGAC GAAGCCCTGC 2332

GGATCCGATG ACTCCTCGCC CGGGGCGATC TCCCGGAGGG GCACCGTTCC GACGTCCGTG 2392

CCATTGCTCA CCCAGGGCTC CCGGCCCCAG CCTTGGGTGT CCGCCGAGAA GAAGAGCAGC 2452

CCGAGATGG CCGTCAGGTT CTCCGGCGAC GCATCCTCGG GGCCCGGCGC CAAATCCTTC 2512

AGCAGCAGGG TGCCCTTGGC GGTGCCATCG CTGGACCACA GCTCCCGGCC GTGGAGGCTG 2572

TCACTCGCGG CGAAGTAGAG CATCCCATTG AGCGCCTTGA TGGCGCTGGG CGCCGAGCTG 2632

TCCGGACCCG GCCAGATGTC CTTACCCCG ACCGTGCCAT GCGACGTGCC ATCGCTGACC 2692

CACAGCTCCT CGCCCTCGGG CTGGCCCCAG AACTCGGGCT CGCCTCCCCC GGCCTGAAG 2752

AAGATCTTCC CCCCAGCGC CGTGAGATCA TCGGATAGA GGCCGGGGAA GAAGCGCAGC 2812

TGCTCGGAGA CGGTGCCTCT GGAGACCAC AGGCTGGCCT CGCCTTCGTC ATTGTCGAGC 2872

AGGAAGAAGA GCACCGAGTC CGCCGCGGTG AACGCGGAGA GGAAGTTGTC CTCGGGGCCC 2932

GTGAAGACAG ACGTGGTGCT GGACAGCCCC AGGCTGCGCC AGATGAACAC CTCGTCATTG 2992

ACGTTGGCCA CGAAGAAGAG CGCATCGCCG ACCCGGGTGA GCCGGCGCGG GCTGGAGCTG 3052

CCGGGCAC 3060

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2788 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..103

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 707..1654

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1644..2591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

T TTC GAG AAG CGC CAT ACC AAA CAG GGG ATA CAG ACC AAC CTG ACG 46
 Phe Glu Lys Arg His Thr Lys Gln Gly Ile Gln Thr Asn Leu Thr
 1 5 10 15

CTG AAA GAG GAA AGC TAC GGC GAC TGG CTG CCG AAG TGC GAC GAC CCC 94
 Leu Lys Glu Glu Ser Tyr Gly Asp Trp Leu Pro Lys Cys Asp Asp Pro
 20 25 30

GCA GCA ACA TAACCTCACT CAGACCGGCA ACAGCCGGTC TTTTCCTTTC 143
 Ala Ala Thr

TGGCCATTGC CACAAGGTGA ACAATCCACT GTTCACCCTT CACCGTTTAT TCACCCITTA 203

TCACTATGAA ATTATTAATA AAAAACCAGA GGTGAACAGT GTGAACAGTA AAACCTGAAA 263

AAACTTTTTTA TCACCCCGCG CATCGCCCGA CTGGACAGAT CCAGAACGAG CAAAAATCAC 323

AAAGGTGACG AGTCGACTGT TCACTCTTCA CCAACTCATC ACCACCTAAC CACATGATAT 383

AAAATGATAA ATAATCGAGG TGAACAGTTA AATGCAAAAA AACTTTTTTET CAGCTCTTGG 443

ATAAAAGAAA ATTAATTCAC ATCAATAGCT TTCCTCTTGA ATCCTCTTGA GGTTTATGAG 503

AGCGTAACAG AGCCAAACCT AGCATTTTAT GGGTTAATAG CCCATCGCGC ATGAGTCATG 563

GTTTCGCCTA GTATTTTAGC TATGCCCGTC GTTCAGTTGG CTGAGCGGCG GCTGGGGGCC 623

ACCGATCAGC GAACTGATCG ACGTGCTCAA GTAGGTTTGG CTCTTTTAGT CCTCTACCAT 683

CAAGGTGCAT AAGGATATTC TCG ATG CTG ACT CAG CTA AAA AAA AAT GGT 733
 Met Leu Thr Gln Leu Lys Lys Asn Gly
 1 5

ACT GAG GTA TCT AGA GCA ACC GCG TTA TTT TCA TCA TTC GTT GAA AAG 781
 Thr Glu Val Ser Arg Ala Thr Ala Leu Phe Ser Ser Phe Val Glu Lys
 10 15 20 25

AAC AAA GTA AAA TGT CCT GGT AAT GTA AAA AAA TTC GTC TTT CTG TGT 829
 Asn Lys Val Lys Cys Pro Gly Asn Val Lys Lys Phe Val Phe Leu Cys
 30 35 40

GGT GCT AAC AAA AAC AAT GGA GAA CCA TCA GCA AGA CGA TTG GAA TTA 877
 Gly Ala Asn Lys Asn Asn Gly Glu Pro Ser Ala Arg Arg Leu Glu Leu
 45 50 55

ATA AAT TTT TCT GAA AGG TAT TTG AAT AAC TGT CAC TTT TTT CTT GCT 925
 Ile Asn Phe Ser Glu Arg Tyr Leu Asn Asn Cys His Phe Phe Leu Ala
 60 65 70

GAA CTA GTT TTC AAA GAA TTA AGC ACC GAT GAA GAA TCA TTA TCT GAT 973
 Glu Leu Val Phe Lys Glu Leu Ser Thr Asp Glu Glu Ser Leu Ser Asp
 75 80 85

AAT TTA TTA GAT ATC GAA GCT GAC TTA TCT AAA TTA GCT GAT CAT ATT 1021
 Asn Leu Leu Asp Ile Glu Ala Asp Leu Ser Lys Leu Ala Asp His Ile
 90 95 100 105

ATC ATT GTT TTA GAA AGT TAT TCA TCT TTC ACG GAA CTT GGT GCA TTC 1069
 Ile Ile Val Leu Glu Ser Tyr Ser Ser Phe Thr Glu Leu Gly Ala Phe
 110 115 120

GCA TAC AGC AAG CAA TTA CGC AAG AAA TTA ATA ATA GTT AAC AAT ACA 1117
 Ala Tyr Ser Lys Gln Leu Arg Lys Lys Leu Ile Ile Val Asn Asn Thr
 125 130 135

AAA TTT ATA AAT GAG AAA TCA TTT ATA AAT ATG GGA CCA ATA AAG GCT Lys Phe Ile Asn Glu Lys Ser Phe Ile Asn Met Gly Pro Ile Lys Ala 140 145 150	1165
ATT ACT CAG CAA TCA CAA CAA TCT GGT CAT TTC TTA CAT TAT AAA ATG Ile Thr Gln Gln Ser Gln Gln Ser Gly His Phe Leu His Tyr Lys Met 155 160 165	1213
ACA GAA GGT ATT GAA AGT ATA GAG CGC TCT GAT GGG ATT GGC GAA ATA Thr Glu Gly Ile Glu Ser Ile Glu Arg Ser Asp Gly Ile Gly Glu Ile 170 175 180 185	1261
TTC GAC CCC CTA TAT GAT ATT CTT TCT AAG AAC GAC AGA GCA ATT TCA Phe Asp Pro Leu Tyr Asp Ile Leu Ser Lys Asn Asp Arg Ala Ile Ser 190 195 200	1309
AGA ACT TTA AAA AAA GAA GAG TTA GAT CCT TCC AGT AAC TTC AAT AAA Arg Thr Leu Lys Lys Glu Glu Leu Asp Pro Ser Ser Asn Phe Asn Lys 205 210 215	1357
GAC TCA GTA CGA TTT ATT CAT GAC GTA ATT TTT GTA TGT GGT CCT TTG Asp Ser Val Arg Phe Ile His Asp Val Ile Phe Val Cys Gly Pro Leu 220 225 230	1405
CAA CTT AAT GAA CTC ATC GAA ATA ATC ACA AAA ATA TTT GGC ACA GAA Gln Leu Asn Glu Leu Ile Glu Ile Ile Thr Lys Ile Phe Gly Thr Glu 235 240 245	1453
AGC CAT TAC AAA AAA AAT CTT CTA AAG CAC CTT GGT ATT CTA ATA GCT Ser His Tyr Lys Lys Asn Leu Leu Lys His Leu Gly Ile Leu Ile Ala 250 255 260 265	1501
ATT AGA ATA ATA TCA TGC ACA AAT GGG ATT TAT TAT TCT TTG TAT AAA Ile Arg Ile Ile Ser Cys Thr Asn Gly Ile Tyr Tyr Ser Leu Tyr Lys 270 275 280	1549
GAA TAT TAT TTT AAA TAT GAC TTT GAC ATT GAC AAC ATA TCA TCA ATG Glu Tyr Tyr Phe Lys Tyr Asp Phe Asp Ile Asp Asn Ile Ser Ser Met 285 290 295	1597
TTT AAA GTT TTT TTC CTC AAG AAC AAG CCA GAA AGG ATG AGG GTA TAT Phe Lys Val Phe Phe Leu Lys Asn Lys Pro Glu Arg Met Arg Val Tyr 300 305 310	1645
GAG AAT ATA TAGCCTAATT GATTCTCAGA CATTGATGAC TAAGGGATT Glu Asn Ile 315	1694
GCTTCTGAAG TAATGCGATC ACCTGAGCCG CCAAAAAAAT GGGATATAGC TAAGAAAAAA	1754
GGAGGTATGA GAACAATTTA TCACCCGTCA TCAAAAGTTA AATTAATTCA ATATTGGTTA	1814
ATGAATAATG TTTTTTCGAA GCTCCCAATG CATAATGCTG CATATGCATT TGTTAAAAAC	1874
CGATCAATAA AAAGCAATGC TTTATTACAT GCCGAATCAA AGAATAAGTA TTATGTGAAA	1934
ATAGATCTCA AAGATTTTTT CCCTTCAATA AAATTTACTG ATTTTGAGTA CGCATTCAC	1994
CGTTATCGAG ATCGCATTGA ATTTACTACA GAATATGATA AGGAGTTACT ACAACTTATA	2054
AAAACGATCT GCTTTATATC AGATAGCACT CTCCCTATCG GGTTTCCTAC ATCTCCATTA	2114
ATTGCAAACT TTGTGGCAAG AGAACTTGAT GAAAACTGA CGCAAAAACT AAATGCAATT	2174

GATAAACTTA ATGCCACTTA TACACGATAT GCTGATGATA TTATTGTCTC TACAAATATG 2234
AAAGGGGCTA GCAAATTAAT TCTGGATTGT TTTAAAAGAA CAATGAAAGA GATTGGTCCA 2294
GACTTTAAAA TTAACATTAA AAAATTTAAG ATTTGTAGTG CTTCGGGAGG AAGTATAGTA 2354
GTTACCGGAT TGAAAGTTTG CCACGATTTT CATATTACAT TACATAGATC AATGAAAGAT 2414
AAAATAAGAT TGCATCTTTC TCTTTTATCA AAGGGCATAT TAAAAGATGA AGATCATAAT 2474
AAACTTTCTG GTTATATTGC TTATGCAAAA GATATAGACC CTCATTTTTA TACAAAACCTG 2534
AACAGAAAAT ATTTTCAAGA AATAAAATGG ATTCAGAATC TCCACAACAA AGTTGAATAA 2594
ACTTTATATT TTGGATGCAC CCCAATAACT TCATTGATTA AATTGGGAAC AATATAGGCT 2654
TTTCAGGATG ACCTACACTC TAGAGAATGT GTATACAAAA GTGTATAAGT TATTTTCAAA 2714
CCTATATAAA ATACAGCAAA ATCAATGCAT TGGCGGCATT TTACCACCTC TGTGATCTTC 2774
CGCCAAAATG CCTC 2788

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Arg Ile Tyr Ser Leu Ile Asp Ser Gln Thr Leu Met Thr Lys Gly
1 5 10 15
Phe Ala Ser Glu Val Met Arg Ser Pro Glu Pro Pro Lys Lys Trp Asp
20 25 30
Ile Ala Lys Lys Lys Gly Gly Met Arg Thr Ile Tyr His Pro Ser Ser
35 40 45
Lys Val Lys Leu Ile Gln Tyr Trp Leu Met Asn Asn Val Phe Ser Lys
50 55 60
Leu Pro Met His Asn Ala Ala Tyr Ala Phe Val Lys Asn Arg Ser Ile
65 70 75 80
Lys Ser Asn Ala Leu Leu His Ala Glu Ser Lys Asn Lys Tyr Tyr Val
85 90 95
Lys Ile Asp Leu Lys Asp Phe Phe Pro Ser Ile Lys Phe Thr Asp Phe
100 105 110
Glu Tyr Ala Phe Thr Arg Tyr Arg Asp Arg Ile Glu Phe Thr Thr Glu
115 120 125
Tyr Asp Lys Glu Leu Leu Gln Leu Ile Lys Thr Ile Cys Phe Ile Ser
130 135 140
Asp Ser Thr Leu Pro Ile Gly Phe Pro Thr Ser Pro Leu Ile Ala Asn
145 150 155 160

Phe Val Ala Arg Glu Leu Asp Glu Lys Leu Thr Gln Lys Leu Asn Ala
 165 170 175
 Ile Asp Lys Leu Asn Ala Thr Tyr Thr Arg Tyr Ala Asp Asp Ile Ile
 180 185 190
 Val Ser Thr Asn Met Lys Gly Ala Ser Lys Leu Ile Leu Asp Cys Phe
 195 200 205
 Lys Arg Thr Met Lys Glu Ile Gly Pro Asp Phe Lys Ile Asn Ile Lys
 210 215 220
 Lys Phe Lys Ile Cys Ser Ala Ser Gly Gly Ser Ile Val Val Thr Gly
 225 230 235 240
 Leu Lys Val Cys His Asp Phe His Ile Thr Leu His Arg Ser Met Lys
 245 250 255
 Asp Lys Ile Arg Leu His Leu Ser Leu Leu Ser Lys Gly Ile Leu Lys
 260 265 270
 Asp Glu Asp His Asn Lys Leu Ser Gly Tyr Ile Ala Tyr Ala Lys Asp
 275 280 285
 Ile Asp Pro His Phe Tyr Thr Lys Leu Asn Arg Lys Tyr Phe Gln Glu
 290 295 300
 Ile Lys Trp Ile Gln Asn Leu His Asn Lys Val Glu
 305 310 315

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1602 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 548..1507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TGGCATCTAT TAAGAAGGTT AGGAAAGAAA ATAAAGTATC AAAAGATATT GGAAATATAT	60
TATACGCAGA GCGTTTCTAT TGCCTTGTAT CTATTTACTG GATAGTGTCA ACTACCGCAC	120
ACTGTGTGAA CTAGCTTTTA AAGCGATAAA GCAAGATGAT GTTTTATCTA AAATTATTGT	180
TAGATCCGTT GTTTCTCGTC TAATAAATGA ACGAAAAATA CTTCAAATGA CTGATGGTTA	240
TCAGGTCAC TCTTTGGGGG CTAGCTATGT TAGGAGCGTC TTTGATAGAA AGACACTTGA	300
CCGATTGCGG CTTGAGATTA TGAATTTTGA AAACCGTAGA AAATCAACAT TTAACATGA	360
TAAGATTCCG TATGCGCACC CTTAGCGAGA GGTATATCAT TAAGGTCAAC CTCTGGATGT	420
TGTTTCGGCA TCCTGCATTG AATCTGAGTT ACTGTCTGTT TTCCTTGTTG GAACGGAGAG	480
CATCGCCTGA TGCTCTCCGA GCCAACCAGG AAACCCGTTT TTTCTGACGT AAGGGTGCAG	540

AACTTTC	ATG	AAA	TCC	GCT	GAA	TAT	TTG	AAC	ACT	TTT	AGA	TTG	AGA	AAT	589	
	Met	Lys	Ser	Ala	Glu	Tyr	Leu	Asn	Thr	Phe	Arg	Leu	Arg	Asn		
	1				5					10						
CTC	GGC	CTA	CCT	GTC	ATG	AAC	AAT	TTG	CAT	GAC	ATG	TCT	AAG	GCG	ACT	637
Leu	Gly	Leu	Pro	Val	Met	Asn	Asn	Leu	His	Asp	Met	Ser	Lys	Ala	Thr	
15				20						25					30	
CGC	ATA	TCT	GTT	GAA	ACA	CTT	CGG	TTG	TTA	ATC	TAT	ACA	GCT	GAT	TTT	685
Arg	Ile	Ser	Val	Glu	Thr	Leu	Arg	Leu	Leu	Ile	Tyr	Thr	Ala	Asp	Phe	
				35				40						45		
CGC	TAT	AGG	ATC	TAC	ACT	GTA	GAA	AAG	AAA	GGC	CCA	GAG	AAG	AGA	ATG	733
Arg	Tyr	Arg	Ile	Tyr	Thr	Val	Glu	Lys	Lys	Gly	Pro	Glu	Lys	Arg	Met	
			50					55					60			
AGA	ACC	ATT	TAC	CAA	CCT	TCT	CGA	GAA	CTT	AAA	GCC	TTA	CAA	GGA	TGG	781
Arg	Thr	Ile	Tyr	Gln	Pro	Ser	Arg	Glu	Leu	Lys	Ala	Leu	Gln	Gly	Trp	
		65					70					75				
GTT	CTA	CGT	AAC	ATT	TTA	GAT	AAA	CTG	TCG	TCA	TCT	CCT	TTT	TCT	ATT	829
Val	Leu	Arg	Asn	Ile	Leu	Asp	Lys	Leu	Ser	Ser	Ser	Pro	Phe	Ser	Ile	
	80					85					90					
GGA	TTT	GAA	AAG	CAC	CAA	TCT	ATT	TTG	AAT	AAT	GCT	ACC	CCG	CAT	ATT	877
Gly	Phe	Glu	Lys	His	Gln	Ser	Ile	Leu	Asn	Asn	Ala	Thr	Pro	His	Ile	
95				100					105						110	
GGG	GCA	AAC	TTT	ATA	CTG	AAT	ATT	GAT	TTG	GAG	GAT	TTT	TTC	CCA	AGT	925
Gly	Ala	Asn	Phe	Ile	Leu	Asn	Ile	Asp	Leu	Glu	Asp	Phe	Phe	Pro	Ser	
				115				120						125		
TTA	ACT	GCT	AAC	AAA	GTT	TTT	GGA	GTG	TTT	CAT	TCT	CTT	GGT	TAT	AAT	973
Leu	Thr	Ala	Asn	Lys	Val	Phe	Gly	Val	Phe	His	Ser	Leu	Gly	Tyr	Asn	
			130				135						140			
CGA	CTA	ATA	TCT	TCA	GTT	TTG	ACA	AAA	ATA	TGT	TGT	TAT	AAA	AAT	CTG	1021
Arg	Leu	Ile	Ser	Ser	Val	Leu	Thr	Lys	Ile	Cys	Cys	Tyr	Lys	Asn	Leu	
		145					150					155				
CTA	CCA	CAA	GGT	GCT	CCA	TCA	TCA	CCT	AAA	TTA	GCT	AAT	CTA	ATA	TGT	1069
Leu	Pro	Gln	Gly	Ala	Pro	Ser	Ser	Pro	Lys	Leu	Ala	Asn	Leu	Ile	Cys	
	160					165					170					
TCT	AAA	CTT	GAT	TAT	CGT	ATT	CAG	GGT	TAT	GCA	GGT	AGT	CGG	GGC	TTG	1117
Ser	Lys	Leu	Asp	Tyr	Arg	Ile	Gln	Gly	Tyr	Ala	Gly	Ser	Arg	Gly	Leu	
175					180				185						190	
ATA	TAT	ACG	AGA	TAT	GCC	GAT	GAT	CTC	ACC	TTA	TCT	GCA	CAG	TCT	ATG	1165
Ile	Tyr	Thr	Arg	Tyr	Ala	Asp	Asp	Leu	Thr	Leu	Ser	Ala	Gln	Ser	Met	
				195				200						205		
AAA	AAG	GTT	GTT	AAA	GCA	CGT	GAT	TTT	TTA	TTT	TCT	ATA	ATC	CCA	AGT	1213
Lys	Lys	Val	Val	Lys	Ala	Arg	Asp	Phe	Leu	Phe	Ser	Ile	Ile	Pro	Ser	
		210					215					220				
GAA	GGA	TTG	GTT	ATT	AAC	TCA	AAA	AAA	ACT	TGT	ATT	AGT	GGG	CCT	CGT	1261
Glu	Gly	Leu	Val	Ile	Asn	Ser	Lys	Lys	Thr	Cys	Ile	Ser	Gly	Pro	Arg	
		225				230					235					
AGT	CAG	AGG	AAA	GTT	ACA	GGT	TTA	GTT	ATT	TCA	CAA	GAG	AAA	GTT	GGG	1309
Ser	Gln	Arg	Lys	Val	Thr	Gly	Leu	Val	Ile	Ser	Gln	Glu	Lys	Val	Gly	
	240					245					250					

ATA GGT AGA GAA AAA TAT AAA GAA ATT AGA GCA AAG ATA CAT CAT ATA 1357
 Ile Gly Arg Glu Lys Tyr Lys Glu Ile Arg Ala Lys Ile His His Ile
 255 260 265 270

TTT TGC GGT AAG TCT TCT GAG ATA GAA CAC GTT AGG GGA TGG TTG TCA 1405
 Phe Cys Gly Lys Ser Ser Glu Ile Glu His Val Arg Gly Trp Leu Ser
 275 280 285

TTT ATT TTA AGT GTG GAT TCA AAA AGC CAT AGG AGA TTA ATA ACT TAT 1453
 Phe Ile Leu Ser Val Asp Ser Lys Ser His Arg Arg Leu Ile Thr Tyr
 290 295 300

ATT AGC AAA TTA GAA AAA AAA TAT GGA AAG AAC CCT TTA AAT AAA GCG 1501
 Ile Ser Lys Leu Glu Lys Lys Tyr Gly Lys Asn Pro Leu Asn Lys Ala
 305 310 315

AAG ACC TAATGGTCTT CGTTTAAAA CTAAAGCTCA TAGGTTGAAA AATTGAGCAC 1557
 Lys Thr
 320

TTCTTCGTCC AACCAGTTAT TTAGTTCCTG CAATCGTTTC TGCAG 1602

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 396..1352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCACCCTGAA AGACCTGATT GCTTACCTGG AAGAGAAGCC GGAAATGGCG GAACATCTGG 60
 CGGCGGTAA GGCCTATCGC GAAGAGTTCG GCGTTTAAAA ATATGCGCTG TGCAGGGTTT 120
 TTGCTGTGCG CAGCGTGATG CGCTTCAAGA TATCGTGTTA ATCTGCTTTC GCCAGCAGTG 180
 GCAATAGCGT TTCCGGCCTT TTGTGCCGGG AGGGTCGGCG AGTCGCTGAC TTAACGCCAG 240
 TAGTATGTCC ATATACCCAA AGTCGCTTCA TTGTACCTGA GTACGCTTCG CGTACGTCGC 300
 GCTGACGCGC TCAGTACAGT TACGCGCCTT CGGGATGGTT TAATGGTATT GCCGCTGTTG 360
 GCGCCTCTTT TGGCCGCCGT GATGTGGAGA GTGGA ATG GAT GCT ACC CGG ACA 413
 Met Asp Ala Thr Arg Thr
 1 5
 ACC CTT CTG GCG CTC GAT TTG TTC GGC TCG CCG GGC TGG AGC GCC GAT 461
 Thr Leu Leu Ala Leu Asp Leu Phe Gly Ser Pro Gly Trp Ser Ala Asp
 10 15 20
 AAA GAA ATA CAG CGA CTG CAT GCG CTC AGT AAT CAT GCC GGA CGC CAT 509
 Lys Glu Ile Gln Arg Leu His Ala Leu Ser Asn His Ala Gly Arg His
 25 30 35

TAC CGA CGC ATT ATT CTT TCT AAA CGC CAC GGT GGT CAG CGG CTG GTG	557
Tyr Arg Arg Ile Ile Leu Ser Lys Arg His Gly Gly Gln Arg Leu Val	
40 45 50	
TTA GCC CCT GAT TAC TTG CTC AAA ACC GTA CAG CGC AAC ATT CTT AAG	605
Leu Ala Pro Asp Tyr Leu Leu Lys Thr Val Gln Arg Asn Ile Leu Lys	
55 60 65 70	
AAC GTC CTT TCA CAA TTT CCG CTT TCC CCT TTT GCT ACA GCC TAC CGA	653
Asn Val Leu Ser Gln Phe Pro Leu Ser Pro Phe Ala Thr Ala Tyr Arg	
75 80 85	
CCA GGT TGC CCA ATC GTC AGC AAC GCG CAG CCA CAC TGC CAA CAG CCG	701
Pro Gly Cys Pro Ile Val Ser Asn Ala Gln Pro His Cys Gln Gln Pro	
90 95 100	
CAG ATC CTG AAA CTC GAT ATC GAA AAC TTT TTC GAT AGC ATT AGC TGG	749
Gln Ile Leu Lys Leu Asp Ile Glu Asn Phe Phe Asp Ser Ile Ser Trp	
105 110 115	
TTA CAG GTC TGG CGT GTG TTT CGC CAG GCC CAG TTG CCA CGT AAT GTG	797
Leu Gln Val Trp Arg Val Phe Arg Gln Ala Gln Leu Pro Arg Asn Val	
120 125 130	
GTA ACC ATG CTG ACC TGG ATT TGT TGT TAT AAC GAC GCG TTA CCG CAG	845
Val Thr Met Leu Thr Trp Ile Cys Cys Tyr Asn Asp Ala Leu Pro Gln	
135 140 145 150	
GGG GCA CCA ACT TCG CCA GCC ATT TCC AAT CTT GTG ATG CGC CGT TTT	893
Gly Ala Pro Thr Ser Pro Ala Ile Ser Asn Leu Val Met Arg Arg Phe	
155 160 165	
GAT GAA CGC ATA GGG GAA TGG TGT CAG GCT CGG GGA ATT ACC TAC ACC	941
Asp Glu Arg Ile Gly Glu Trp Cys Gln Ala Arg Gly Ile Thr Tyr Thr	
170 175 180	
CGC TAC TGC GAT GAC ATG ACC TTT TCA GGT CAC TTC AAT GCC CGC CAG	989
Arg Tyr Cys Asp Asp Met Thr Phe Ser Gly His Phe Asn Ala Arg Gln	
185 190 195	
GTT AAA AAT AAA GTG TGC GGA TTG TTA GCG GAG CTG GGC CTG AGC CTC	1037
Val Lys Asn Lys Val Cys Gly Leu Leu Ala Glu Leu Gly Leu Ser Leu	
200 205 210	
AAT AAA CGC AAA GGC TGC CTG ATA GCT GCC TGT AAG CGC CAG CAA GTA	1085
Asn Lys Arg Lys Gly Cys Leu Ile Ala Ala Cys Lys Arg Gln Gln Val	
215 220 225 230	
ACC GGG ATT GTT GTT AAT CAC AAG CCA CAG CTT GCC CGT GAA GCG CGC	1133
Thr Gly Ile Val Val Asn His Lys Pro Gln Leu Ala Arg Glu Ala Arg	
235 240 245	
CGG GCG CTG CGT CAG GAG GTG CAT TTG TGC CAA AAA TAT GGC GTT ATT	1181
Arg Ala Leu Arg Gln Glu Val His Leu Cys Gln Lys Tyr Gly Val Ile	
250 255 260	
TCG CAT CTT AGT CAT CGT GGT GAA CTT GAT CCT TCT GGC GAT CTC CAC	1229
Ser His Leu Ser His Arg Gly Glu Leu Asp Pro Ser Gly Asp Leu His	
265 270 275	
GCA CAG GCA ACG GCG TAT CTT TAT GCT TTG CAG GGA AGA ATA AAC TGG	1277
Ala Gln Ala Thr Ala Tyr Leu Tyr Ala Leu Gln Gly Arg Ile Asn Trp	
280 285 290	

TTA TTG CAA ATC AAC CCT GAG GAT GAG GCC TTT CAA CAG GCG AGA GAG 1325
Leu Leu Gln Ile Asn Pro Glu Asp Glu Ala Phe Gln Gln Ala Arg Glu
295 300 305 310

AGT GTA AAG CGA ATG CTG GTT GCA TGG TAAGAAAAGC GTCAGGCAGA 1372
Ser Val Lys Arg Met Leu Val Ala Trp
315

CGTTTCTGCC TGACCGTTTA GGGGAGAATT ACTGCAACTG CGCGGCAATT AGCGGCCAGC 1432

GGGCGTCAAA ATCATCCGTC GGGCGGTATT TAAACTCGCT GCGGACAAA CGTGACAGCA 1492

TACCTTCACA GAAGGCCAGG ATCTGGCTTG CCAGCAGGGT TTCATCGG 1540

61